

ABSTRACT

General methods of biological sample classification based on gene expression analysis are described. The methods segregate individual samples into distinct classes using quantitative measurements of expression values for selected sets of genes in individual samples compared to a reference standard. Samples displaying positive and negative correlations of the gene expression values with the reference standard samples exhibit distinct behaviors and pathohistological features. Also disclosed are methods for identifying sets of genes whose expression patterns are correlated with a phenotype. Such sets are useful for characterizing cellular differentiation pathways and states and for identifying potential drug discovery targets.

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